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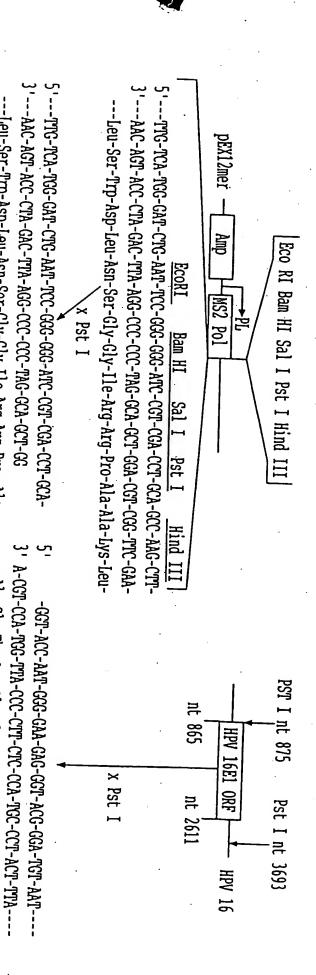
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---Leu-Ser-Trp-Asp-Leu-Asn-Ser-Gly-Gly-Ile-Arg-Arg-Pro--Ala

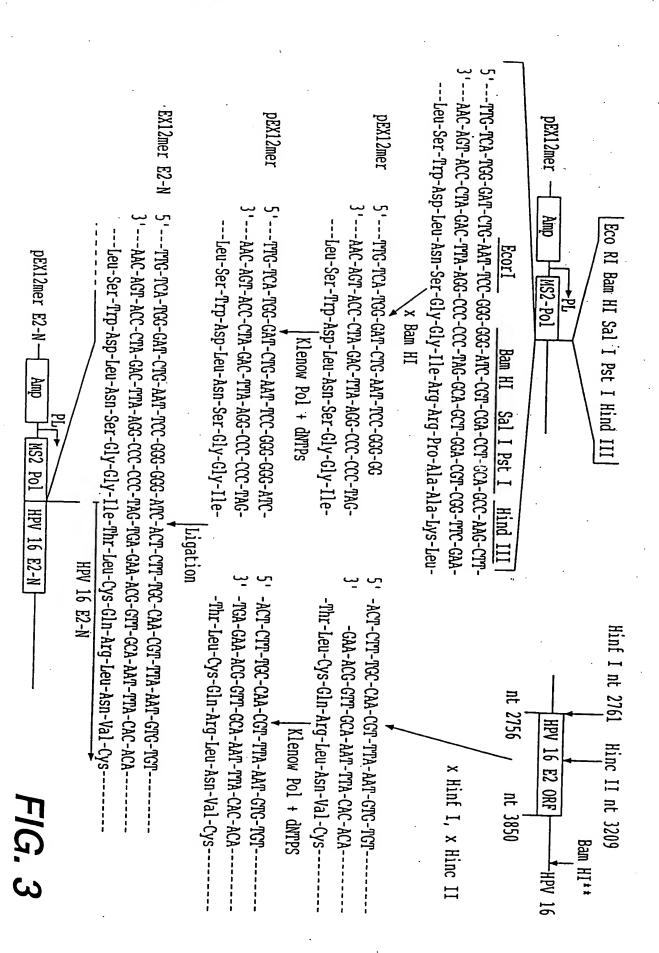
Ligation

Ala-Gly-Thr-Asn-Gly-Glu-Glu-Gly-Thr-Gly-Cys-Asn---

EX12merE1 5'----TTG-TCA-TGG-GAT-CTG-AAT-TCC-GGG-GGG-ATC-CGT-CGA-CCT-GCA-GGT-ACC-AAT-GGG-GAA-GAG-GGT-ACG-GGA-TGT-AAT---3'----AAC-AGT-ACC-CTA-GAC-TTA-AGG-CCC-CCC-TAG-GCA-GCT-GGA-CGT-CCA-TGG-TTA-CCC-CTT-CTC-CCA-TGC-CCT-ACA-TTA----Leu-Ser-Trp-Asp-Leu-Asn-Ser-Gly-Gly-Ile-Arg-Arg-Pro-Ala-Gly-Thr-Asn-Gly-Glu-Glu-Gly-Thr-Gly-Cys-Asn--pEX12merE1 Amp MS2-Pol HPV 16 E1 HPV 16 E1

r —	CLONE SEQUENCE	POSITION	ISOLATE
	REGION E1-1090:		
	1090 NGWFYVEAVVEKKTGDAISDDENENDSDTGEDLVDFIVNDNDYLT	As 16-60	-
	1079 NENDSDTGEDLVDFIVND	AS 38-55	ω
	1084 MADPAGTINGEEGTGCNGHFYVEAVVEKKTGDAISDDENENDSDTGEDLVDFIVNDNDYLT	AS 1-60	<u>س</u>
	1029 EDLVDFIVNDNDYLT	AS 46-60	<u>~</u>
	1099	AS 46-79	5
	1145 NENDSDTGEDLVDFTVNDNDYLTQAETETAHALFTAQEAKQHRDAVQVLKRKYLvvh	AS 38-91	
·	REGION E1-1059:		
	stgsktkvfGSPLSDIS	AS 92-99	

FIG. 2



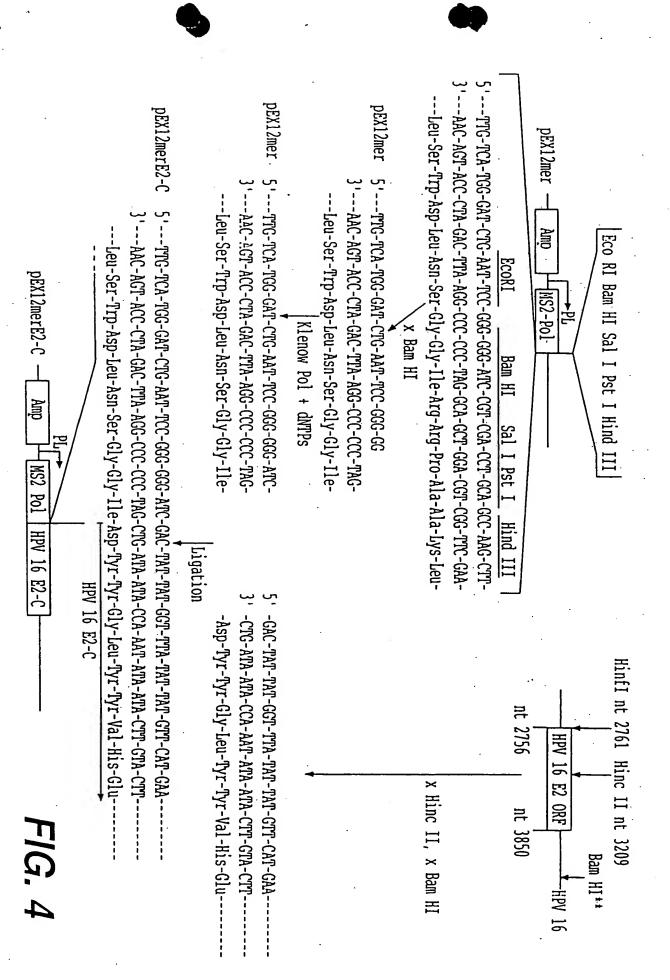


FIG. 5

~	AS 231-249	TEETQTTIQRPRSEPDIGN	1091
	AS 209-245	EI IROHLANHPAATHTKAVALGTEETQTTIQRPRSEP	REGION E2-1102: 1102
2	AS 199-234	VFSSNEVSSPEIIRQHLANHPAATHTKAVALGTEET	1121
	AS 197-211	TSVFSSNEVSSPEII	1158
			REGION E2-1158:
-	AS 78-91	TLETIYNSQYSNEK	1156
-	AS 76-100	QLTLETI YNSQYSNEKWTLQDVSLE	1112
			REGION E2-1112:
2	AS 61-76	TLAVSKNKALQAIELQLTLETIYNSQYSNEKWTLQDV	1018
4	AS 55-70	INHQVVPTLAVSKNKAL	1057
-	AS 55-73	INHQVVPTLAVSKNKALQAI	1063
	AS 43-67	YYKAREMGFKHINHQVVPTLAVSKN	1061
2	AS 41-70	AIYYKARENGFKHINHQVVPTLAVSKNKAL	1060
4	AS 41-63	AIYYKAREMGFKHINHQVVPTLA	1074
			REGION E2-1074:
2	AS 25-35	DLRDHIDYWKH	1170
			REGION E2-1170:
5	AS 13-30	STDLRDHI	1025 DKILTHYENDSTDLRDHI
w	AS 13-23	S	1066 DKILTHYENDS
-			REGION E2-1066:
ISOLATE	POSITION	SEQUENCE	CLONE